



079-us1.ST25.txt

SEQUENCE LISTING

<110> Paz Einat, Louis Deiss and Ruth Maya  
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Val Asn Asp Leu Ile His Gly Lys Asn Gly Leu Leu Phe Thr Tyr Gly  
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## 079-us1.ST25.txt

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tat aaa aca agg ggt ggt gga caa tct gtt cag ttt act gat att gag	2688
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775

780

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Glu Lys Ala Leu Ala Lys Cys Glu Lys Tyr Met Leu Thr His Gln Glu  
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Tyr Lys Thr Arg Gly Gly Gly Gln Ser Val Gln Phe Thr Asp Ile Glu  
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aat aca act gtt cag ctt cat act cct gag ggc tac aga ctc aac cga 309  
 Asn Thr Thr Val Gln Leu His Thr Pro Glu Gly Tyr Arg Leu Asn Arg  
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## 079-us1.ST25.txt

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Ser Phe Gln Ala Lys Arg Tyr Val Phe Lys Ser Asn Asp Arg Asn Ser	
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Met Asp Ile Gln Cys Glu Val Asp Ala Leu Leu Glu Arg Gln Lys Arg	
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Glu Ala Met Pro Asn Pro Lys Thr Ser Ser Ser Lys Arg Gln Val Asp	
180 185 190	
cca gag ttt gca gat atg ata act gta caa gaa ttc tgc aaa gca gaa	741
Pro Glu Phe Ala Asp Met Ile Thr Val Gln Glu Phe Cys Lys Ala Glu	
195 200 205	
gag gtt gat gaa gat agt gtc tat ggt gta ttt gtc tct tat att gaa	789
Glu Val Asp Glu Asp Ser Val Tyr Gly Val Phe Val Ser Tyr Ile Glu	
210 215 220	
ata tat aat aat tac ata tat gat cta ttg gaa gag gtg ccg ttt gat	837
Ile Tyr Asn Asn Tyr Ile Tyr Asp Leu Leu Glu Glu Val Pro Phe Asp	
225 230 235 240	
ccc ata aaa ccc aaa cct cca caa tct aaa ttg ctt cgt gaa gat aag	885
Pro Ile Lys Pro Lys Pro Pro Gln Ser Lys Leu Leu Arg Glu Asp Lys	
245 250 255	
aac cat aac atg tat gtt gca gga tgt aca gaa gtt gaa gtg aaa tct	933
Asn His Asn Met Tyr Val Ala Gly Cys Thr Glu Val Glu Val Lys Ser	
260 265 270	
act gag gag gct ttt gaa gtt ttc tgg aga ggc cag aaa aag aga cgt	981
Thr Glu Glu Ala Phe Glu Val Phe Trp Arg Gly Gln Lys Lys Arg Arg	
275 280 285	
att gct aat acc cat ttg aat cgt gag tcc agc cgt tcc cat agc gtg	1029
Ile Ala Asn Thr His Leu Asn Arg Glu Ser Ser Arg Ser His Ser Val	
290 295 300	
ttc aac att aaa tta gtt cag gct ccc ttg gat gca gat gga gac aat	1077
Phe Asn Ile Lys Leu Val Gln Ala Pro Leu Asp Ala Asp Gly Asp Asn	
305 310 315 320	
gtc tta cag gaa aaa gaa caa atc act ata agt cag ttg tcc ttg gta	1125
Val Leu Gln Glu Lys Glu Gln Ile Thr Ile Ser Gln Leu Ser Leu Val	
325 330 335	
gat ctt gct gga agt gaa aga act aac cgg acc aga gca gaa ggg aac	1173
Asp Leu Ala Gly Ser Glu Arg Thr Asn Arg Thr Arg Ala Glu Gly Asn	
340 345 350	
aga tta cgt gaa gct ggt aat att aat cag tca cta atg acg cta aga	1221
Arg Leu Arg Glu Ala Gly Asn Ile Asn Gln Ser Leu Met Thr Leu Arg	
355 360 365	

## 079-us1.ST25.txt

aca tgt atg gat gtc cta aga gag aac caa atg tat gga act aac aag Thr Cys Met Asp Val Leu Arg Glu Asn Gln Met Tyr Gly Thr Asn Lys 370 375 380	1269
atg gtt cca tat cga gat tca aag tta acc cat ctg ttc aag aac tac Met Val Pro Tyr Arg Asp Ser Lys Leu Thr His Leu Phe Lys Asn Tyr 385 390 395 400	1317
ttt gat ggg gaa gga aaa gtg cgg atg atc gtg tgt gtg aac ccc aag Phe Asp Gly Glu Gly Lys Val Arg Met Ile Val Cys Val Asn Pro Lys 405 410 415	1365
gct gaa gat tat gaa gaa aac ttg caa gtc atg aga ttt gcg gaa gtg Ala Glu Asp Tyr Glu Glu Asn Leu Gln Val Met Arg Phe Ala Glu Val 420 425 430	1413
act caa gaa gtt gaa gta gca aga cct gta gac aag gca ata tgt ggt Thr Gln Glu Val Glu Val Ala Arg Pro Val Asp Lys Ala Ile Cys Gly 435 440 445	1461
tta acg cct ggg agg aga tac aga aac cag cct cga ggt cca gtt gga Leu Thr Pro Gly Arg Arg Tyr Arg Asn Gln Pro Arg Gly Pro Val Gly 450 455 460	1509
aat gaa cca ttg gtt act gac gtg gtt ttg cag agt ttt cca cct ttg Asn Glu Pro Leu Val Thr Asp Val Val Leu Gln Ser Phe Pro Pro Leu 465 470 475 480	1557
ccg tca tgc gaa att ttg gat atc aac gat gag cag aca ctt cca agg Pro Ser Cys Glu Ile Leu Asp Ile Asn Asp Glu Gln Thr Leu Pro Arg 485 490 495	1605
ctg att gaa gcc tta gag aaa cga cat aac tta cga caa atg atg att Leu Ile Glu Ala Leu Glu Lys Arg His Asn Leu Arg Gln Met Met Ile 500 505 510	1653
gat gag ttt aac aaa caa tct aat gct ttt aaa gct ttg tta caa gaa Asp Glu Phe Asn Lys Gln Ser Asn Ala Phe Lys Ala Leu Leu Gln Glu 515 520 525	1701
ttt gac aat gct gtt tta agt aaa gaa aac cac atg caa ggg aaa cta Phe Asp Asn Ala Val Leu Ser Lys Glu Asn His Met Gln Gly Lys Leu 530 535 540	1749
aat gaa aag gag aag atg atc tca gga cag aaa ttg gaa ata gaa cga Asn Glu Lys Glu Lys Met Ile Ser Gly Gln Lys Leu Glu Ile Glu Arg 545 550 555 560	1797
ctg gaa aag aaa aac aaa act tta gaa tat aag att gag att tta gag Leu Glu Lys Lys Asn Lys Thr Leu Glu Tyr Lys Ile Glu Ile Leu Glu 565 570 575	1845
aaa aca act act atc tat gag gaa gat aaa cgc aat ttg caa cag gaa Lys Thr Thr Thr Ile Tyr Glu Glu Asp Lys Arg Asn Leu Gln Gln Glu 580 585 590	1893
ctt gaa act cag aac cag aaa ctt cag cga cag ttt tct gac aaa cgc Leu Glu Thr Gln Asn Gln Lys Leu Gln Arg Gln Phe Ser Asp Lys Arg	1941

## 079-us1.ST25.txt

595	600	605	
aga tta gaa gcc agg ttg caa ggc atg gtg aca gaa acg aca atg aag Arg Leu Glu Ala Arg Leu Gln Gly Met Val Thr Glu Thr Thr Met Lys 610 615 620			1989
tgg gag aaa gaa tgt gag cgt aga gtg gca gcc aaa cag ctg gag atg Trp Glu Lys Glu Cys Glu Arg Arg Val Ala Ala Lys Gln Leu Glu Met 625 630 635 640			2037
cag aat aaa ctc tgg gtt aaa gat gaa aag ctg aaa caa ctg aag gct Gln Asn Lys Leu Trp Val Lys Asp Glu Lys Leu Lys Gln Leu Lys Ala 645 650 655			2085
att gtt act gaa cct aaa act gag aag cca gag aga ccc tct cgg gag Ile Val Thr Glu Pro Lys Thr Glu Lys Pro Glu Arg Pro Ser Arg Glu 660 665 670			2133
cga gat cga gaa aaa gtt act caa aga tct gtt tct cca tca cct gtg Arg Asp Arg Glu Lys Val Thr Gln Arg Ser Val Ser Pro Ser Pro Val 675 680 685			2181
cct tta ctc ttt caa cct gat cag aac gca cca cca att cgt ctc cga Pro Leu Leu Phe Gln Pro Asp Gln Asn Ala Pro Pro Ile Arg Leu Arg 690 695 700			2229
cac aga cga tca cgc tct gca gga gac aga tgg gta gat cat aag ccc His Arg Arg Ser Arg Ser Ala Gly Asp Arg Trp Val Asp His Lys Pro 705 710 715 720			2277
gcc tct aac atg caa act gaa aca gtc atg cag cca cat gtc cct cat Ala Ser Asn Met Gln Thr Glu Thr Val Met Gln Pro His Val Pro His 725 730 735			2325
gcc atc aca gta tct gtt gca aat gaa aag gca cta gct aag tgt gag Ala Ile Thr Val Ser Val Ala Asn Glu Lys Ala Leu Ala Lys Cys Glu 740 745 750			2373
aag tac atg ctg acc cac cag gaa cta gcc tcc gat ggg gag att gaa Lys Tyr Met Leu Thr His Gln Glu Leu Ala Ser Asp Gly Glu Ile Glu 755 760 765			2421
act aaa cta att aag ggt gat att tat aaa aca agg ggt ggt gga caa Thr Lys Leu Ile Lys Gly Asp Ile Tyr Lys Thr Arg Gly Gly Gly Gln 770 775 780			2469
tct gtt cag ttt act gat att gag act tta aag caa gaa tca cca aat Ser Val Gln Phe Thr Asp Ile Glu Thr Leu Lys Gln Glu Ser Pro Asn 785 790 795 800			2517
ggt agt cga aaa cga aga tct tcc aca gta gca cct gcc caa cca gat Gly Ser Arg Lys Arg Arg Ser Ser Thr Val Ala Pro Ala Gln Pro Asp 805 810 815			2565
ggt gca gag tct gaa tgg acc gat gta gaa aca agg tgt tct gtg gct Gly Ala Glu Ser Glu Trp Thr Asp Val Glu Thr Arg Cys Ser Val Ala 820 825 830			2613
gtg gag atg aga gca gga tcc cag ctg gga cct gga tat cag cat cac			2661

079-us1.ST25.txt

Val	Glu	Met	Arg	Ala	Gly	Ser	Gln	Leu	Gly	Pro	Gly	Tyr	Gln	His	His	
		835					840					845				
gca caa ccc aag cgc aaa aag cca tga actgacagtc ccagtactga															2708	
Ala	Gln	Pro	Lys	Arg	Lys	Lys	Pro									
		850				855										
aagaacattt tcatttgtgt ggatgatttc tcgaaagcca tgccagaagc agtcttccag															2768	
gtcatcttgt agaactccag ctttgttgaa aatcacggac ctcagctaca tcatacactg															2828	
accagagca aagctttccc tatggttcca aagacaacta gtattcaaca aaccttgtat															2888	
agtatatgtt ttgccatatt taatattaat agcagaggaa gactcctttt ttcatacactg															2948	
tatgaatttt ttataatgtt tttttaaaat atatttcatg tataacttata aactaattca															3008	
cacaagtgtt tgtcttagat gattaaggaa gactatatct agatcatgtc tgatttttta															3068	
ttgtgacttc tccagccctg gtctgaattt cttaaggttt tataaacaaa tgctgctatt															3128	
tattagctgc aagaatgcac tttagaacta tttgacaatt cagactttca aaataaagat															3188	
gtaaagtact ggccaataat aaccatttta ggaaggtgtt ttgaattctg tatgtatata															3248	
ttcactttct gacattttaga tatgccaaaa gaattaaaat caaaagcact aagaaataaa															3308	
aaaaaaaaaa aaaaaa															3324	

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 <213> Homo sapiens

<400> 6

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20 25 30															
Arg Pro Leu Gly Phe Pro Asp Gln Glu Cys Cys Ile Glu Val Ile Asn															
35 40 45															
Asn Thr Thr Val Gln Leu His Thr Pro Glu Gly Tyr Arg Leu Asn Arg															
50 55 60															
Asn Gly Asp Tyr Lys Glu Thr Gln Tyr Ser Phe Lys Gln Val Phe Gly															
65 70 75 80															
Thr His Thr Thr Gln Lys Glu Leu Phe Asp Val Val Ala Asn Pro Leu															
85 90 95															

Val Asn Asp Leu Ile His Gly Lys Asn Gly Leu Leu Phe Thr Tyr Gly  
 100 105 110

Val Thr Gly Ser Gly Lys Thr His Thr Met Thr Gly Ser Pro Gly Glu  
 115 120 125

Gly Gly Leu Leu Pro Arg Cys Leu Asp Met Ile Phe Asn Ser Ile Gly  
 130 135 140

Ser Phe Gln Ala Lys Arg Tyr Val Phe Lys Ser Asn Asp Arg Asn Ser  
 145 150 155 160

Met Asp Ile Gln Cys Glu Val Asp Ala Leu Leu Glu Arg Gln Lys Arg  
 165 170 175

Glu Ala Met Pro Asn Pro Lys Thr Ser Ser Ser Lys Arg Gln Val Asp  
 180 185 190

Pro Glu Phe Ala Asp Met Ile Thr Val Gln Glu Phe Cys Lys Ala Glu  
 195 200 205

Glu Val Asp Glu Asp Ser Val Tyr Gly Val Phe Val Ser Tyr Ile Glu  
 210 215 220

Ile Tyr Asn Asn Tyr Ile Tyr Asp Leu Leu Glu Glu Val Pro Phe Asp  
 225 230 235 240

Pro Ile Lys Pro Lys Pro Pro Gln Ser Lys Leu Leu Arg Glu Asp Lys  
 245 250 255

Asn His Asn Met Tyr Val Ala Gly Cys Thr Glu Val Glu Val Lys Ser  
 260 265 270

Thr Glu Glu Ala Phe Glu Val Phe Trp Arg Gly Gln Lys Lys Arg Arg  
 275 280 285

Ile Ala Asn Thr His Leu Asn Arg Glu Ser Ser Arg Ser His Ser Val  
 290 295 300

Phe Asn Ile Lys Leu Val Gln Ala Pro Leu Asp Ala Asp Gly Asp Asn  
 305 310 315 320

Val Leu Gln Glu Lys Glu Gln Ile Thr Ile Ser Gln Leu Ser Leu Val

Asp Leu Ala Gly Ser Glu Arg Thr Asn Arg Thr Arg Ala Glu Gly Asn  
 340 345 350

Arg Leu Arg Glu Ala Gly Asn Ile Asn Gln Ser Leu Met Thr Leu Arg  
 355 360 365

Thr Cys Met Asp Val Leu Arg Glu Asn Gln Met Tyr Gly Thr Asn Lys  
 370 375 380

Met Val Pro Tyr Arg Asp Ser Lys Leu Thr His Leu Phe Lys Asn Tyr  
 385 390 395 400

Phe Asp Gly Glu Gly Lys Val Arg Met Ile Val Cys Val Asn Pro Lys  
 405 410 415

Ala Glu Asp Tyr Glu Glu Asn Leu Gln Val Met Arg Phe Ala Glu Val  
 420 425 430

Thr Gln Glu Val Glu Val Ala Arg Pro Val Asp Lys Ala Ile Cys Gly  
 435 440 445

Leu Thr Pro Gly Arg Arg Tyr Arg Asn Gln Pro Arg Gly Pro Val Gly  
 450 455 460

Asn Glu Pro Leu Val Thr Asp Val Val Leu Gln Ser Phe Pro Pro Leu  
 465 470 475 480

Pro Ser Cys Glu Ile Leu Asp Ile Asn Asp Glu Gln Thr Leu Pro Arg  
 485 490 495

Leu Ile Glu Ala Leu Glu Lys Arg His Asn Leu Arg Gln Met Met Ile  
 500 505 510

Asp Glu Phe Asn Lys Gln Ser Asn Ala Phe Lys Ala Leu Leu Gln Glu  
 515 520 525

Phe Asp Asn Ala Val Leu Ser Lys Glu Asn His Met Gln Gly Lys Leu  
 530 535 540

Asn Glu Lys Glu Lys Met Ile Ser Gly Gln Lys Leu Glu Ile Glu Arg  
 545 550 555 560



## 079-us1.ST25.txt

Leu Glu Lys Lys Asn Lys Thr Leu Glu Tyr Lys Ile Glu Ile Leu Glu  
 565 570 575

Lys Thr Thr Thr Ile Tyr Glu Glu Asp Lys Arg Asn Leu Gln Gln Glu  
 580 585 590

Leu Glu Thr Gln Asn Gln Lys Leu Gln Arg Gln Phe Ser Asp Lys Arg  
 595 600 605

Arg Leu Glu Ala Arg Leu Gln Gly Met Val Thr Glu Thr Thr Met Lys  
 610 615 620

Trp Glu Lys Glu Cys Glu Arg Arg Val Ala Ala Lys Gln Leu Glu Met  
 625 630 635 640

Gln Asn Lys Leu Trp Val Lys Asp Glu Lys Leu Lys Gln Leu Lys Ala  
 645 650 655

Ile Val Thr Glu Pro Lys Thr Glu Lys Pro Glu Arg Pro Ser Arg Glu  
 660 665 670

Arg Asp Arg Glu Lys Val Thr Gln Arg Ser Val Ser Pro Ser Pro Val  
 675 680 685

Pro Leu Leu Phe Gln Pro Asp Gln Asn Ala Pro Pro Ile Arg Leu Arg  
 690 695 700

His Arg Arg Ser Arg Ser Ala Gly Asp Arg Trp Val Asp His Lys Pro  
 705 710 715 720

Ala Ser Asn Met Gln Thr Glu Thr Val Met Gln Pro His Val Pro His  
 725 730 735

Ala Ile Thr Val Ser Val Ala Asn Glu Lys Ala Leu Ala Lys Cys Glu  
 740 745 750

Lys Tyr Met Leu Thr His Gln Glu Leu Ala Ser Asp Gly Glu Ile Glu  
 755 760 765

Thr Lys Leu Ile Lys Gly Asp Ile Tyr Lys Thr Arg Gly Gly Gly Gln  
 770 775 780

Ser Val Gln Phe Thr Asp Ile Glu Thr Leu Lys Gln Glu Ser Pro Asn  
 785 790 795 800

079-us1.ST25.txt

Gly Ser Arg Lys Arg Arg Ser Ser Thr Val Ala Pro Ala Gln Pro Asp  
805 810 815

Gly Ala Glu Ser Glu Trp Thr Asp Val Glu Thr Arg Cys Ser Val Ala  
820 825 830

Val Glu Met Arg Ala Gly Ser Gln Leu Gly Pro Gly Tyr Gln His His  
835 840 845

Ala Gln Pro Lys Arg Lys Lys Pro  
850 855

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<212> DNA  
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tcccagtact gaaagaacat ttccatttgt gtggatgatt tctcgaaagc catgccagaa 120  
gcagtcttcc aggtcatctt gtagaactcc agctttgtta aaatcacgga cctcagctac 180  
atcatacact gaccagagc a 201